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GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 9, 2002, 07:32:20 ; Search time 2740 Seconds

(without alignments)
2018.078 Million cell updates/sec

Title: US-09-895-298A-83

Perfect score: 190
Sequence: 1 MANFOPPSKMRASQMMTF.....HGSGLDKRRSRVQEGNPRA 190

Scoring table:

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Ygapop 60.0 Ygapext 60.0
Fgapop 6.0 Fgapext 7.0
Delop 6.0 Delext 7.0

Searched: 2054640 segs, 14551402878 residues

Word size: 4

Total number of hits satisfying chosen parameters: 2253933

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	190	100.0	1219	6 AX108540	AX108540 Homo sapi
2	190	100.0	1813	9 AK023655	AK023655 Homo sapi
3	190	100.0	1960	6 AX108538	AX108538 Homo sapi
4	190	100.0	2407	6 AX108534	AX108534 Sequence
5	190	100.0	2521	6 AX108536	AX108536 Sequence
6	190	100.0	2760	6 BC027602	BC027602 Homo sapi
7	135	71.1	2387	9 AK093944	AK093944 Homo sapi
8	126	66.3	2399	9 AK097718	AK097718 Homo sapi
9	59	31.1	220633	9 HU091321	U91321 Human Chrom
10	59	31.1	223280	2 AC130456	AC130456 Homo sapi
11	35	18.4	164564	9 HBCAC003108	AC003108 Human Chr
12	25	13.2	110000	2 AC124444.2	Continuation (3 of
13	18	9.5	623	10 MM0297000	AC108877 Mus muscu
14	17	8.9	71596	2 AC100877	AC100877 Mus muscu
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17	10	5.3	4790	1 STYARABAD	M11047 S. Typhimuri
18	10	5.3	20558	1 AE008698	AE008698 Salmonell
19	10	5.3	91692	2 CNS0869G	AL732641 Oryza sat
20	10	5.3	150789	9 HS21E7	AL033375 Human DNA
21	10	5.3	163876	2 AC094128	AC094128 Rattus no
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25	9	4.7	330	6 AX135333	AX135333 Sequence
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27	9	4.7	1949	8 AROARAH	L38853 Atrachis hyp
28	9	4.7	12907	1 ARO11768	AE011768 Xanthomon
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30	9	4.7	76967	9 AC008475	AC008475 Homo sapi
31	9	4.7	88065	9 AP002015	AP002015 Homo sapi
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33	9	4.7	95616	9 AC104655	AC104655 Homo sapi
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37	9	4.7	110441	2 HS23	Z82169 Homo sapien
38	9	4.7	113116	2 AC094341	AC094341 Rattus no
39	9	4.7	115833	2 AC099324	AC099324 Oryza sat
40	9	4.7	116758	2 AP004134	AP004134 Oryza sat
41	9	4.7	120126	2 AC087096	AC087096 Oryza sat
42	9	4.7	122167	2 AP005302	AP005302 Oryza sat
43	9	4.7	122288	9 AL359384	AL359384 Human DNA
44	9	4.7	123620	8 AC103891	AC103891 Oryza sat
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RESULT 1

ALIGNMENTS

AXI08540	LOCUS	AXI08540	1219 bp	DNA	linear	PAT 30-APR-2001
AXI08540	DEFINITION	Sequence 7 from Patent WO0123417.				
AXI08540	ACCESSION	AXI08540				
AXI08540.1	VERSION	GI:13923839				
KEYWORDS	SOURCE	human.				
ORGANISM	SOURCE	human.				
REFERENCE	AUTHORS	Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 1219)				
TITLE	AUTHORS	Vinals y de Bassols, C.				
JOURNAL	AUTHORS	Human tumor-associated lak-4p related polynucleotides and peptides and their uses				
FEATURES	Location/Qualifiers	Patent: WO 0123417-A 7 05-APR-2001; SMITHKLINE BEECHAM BIOLOGICALS S.A. (BE)				
BASE COUNT	346 a	260 c	275 g	338 t		
ALIGNMENT SCORES:						
Pred. No.:	2.4e-189	Length:	1219			
Score:	190.00	Matches:	190			
Percent Similarity:	100.00%	Conservative:	0			
Best Local Similarity:	100.00%	Mismatches:	0			
Query Match:	100.00%	Indels:	0			
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Db	4	ATGATGATTTTCACACCTCCGAGCAACACCTGGGGGCTCAGATGATATGATCTTCTTC	63			
QY	21	IllePheLeuLeuPhePheProSerPheThrGlyValLeuCysThrIleAlaIleThrIle	40			
Db	64	ATCTCTTCTGCTTTTCCATCTTTCACGGGGGCTTGTGACCCCTGGCCATCCATC	123			
QY	41	TrpArgLeuIysProSerAlaAspCysGlyTrpPheArgGlyLeuProLeuPheIleHis	60			
Db	124	TGGAGATTGAAGCCCTTCAGCTGAGTGGCCCTTTTCAGAGCTGCGCTCTTCATTCAC	183			
QY	61	SerIleIysSerTrpIleAspThrLeuSerThrArgProGlyTrpIleuTrpValIleTrp	80			
Db	184	TCCATCTACACCTGATGACACCCCTTANGTACAGGGCTGGCTACCTGGGGTGGTGG	243			
QY	81	IlleIysArgAsnLeuIleGlySerValHisPhePheIleIleuThrIleValIleu	100			
Db	244	ATCTATCGAAGCCTCATTTGGAAGTGTGCATCTTTTTCATCCCTACCCCTCATTTGCTG	303			
QY	101	IlleIleThrTrpLeuIysTrpGlnIleThrGluGlyArgIleMetIleArgLeuIleu	120			
Db	304	ATCTATCAACCTATCTTCTTACTGGCAGATCAGAGAGGGAAGATTATGATAGAGCTGCTC	363			
QY	121	HisGlnGlnIleIleAsnGlnGlyIlyAspIlySerPheLeuIleGlyIlySleuIleIys	140			
Db	364	CATAGCAGATCATTAATATGAGGGCAAGATTAATATGTTCTCTGATAGAAAATTGATCAG	423			
QY	141	LeuGlnAspMetGlyIlySlyAlaAsnProSerSerLeuValleuGlnArgGluVal	160			
Db	424	CTGAGAGATATGGAAGAAAGCAAAACCCAGCTCACTTTTCTGGAAAAGAGAGAGTG	483			
QY	161	GluGlnGlnGlyPheLeuHisLeuGlyGlnHisAspIlySerLeuAspLeuArgSerArg	180			
Db	484	GAGCAACAAAGCTTTTTCATTTTGGGGGAACATGATGACAGTCTGTGACTGGCGATGAGA	543			
QY	181	ArgSerValGlnGlnGlyAsnProArgAla	190			
Db	544	AGATCACTTAAAGAGGTAAATCCAAAGGGCC	573			

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RESULT 2
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LOCUS AK023655 1813 bp mRNA linear PRI 01-AUG-2002
DEFINITION Homo sapiens CDNA FLJ13593 fis, clone PLACE1009493.
ACCESSION AK023655
VERSION AK023655.1 GI:10435644
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens placenta cDNA to mRNA, clone_1lb:PLACE1
clone:PLACE1009493.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y.,
Nishikawa,T., Nagai,K., Sugano,S., Shiratori,A., Sudo,H.,
Wagatsuma,M., Hosohiri,T., Kaku,Y., Kodaira,H., Kondo,H.,
Sugawara,M., Takahashi,M., Chiba,Y., Ishida,S., Murakawa,K.,
Ono,Y., Takiguchi,S., Watanabe,S., Kimura,K., Murakami,K.,
Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A.,
Nakamura,Y., Nagahara,K., Masubo,Y., Ninomiya,K. and Iwayanagi,T.
MEDO human cDNA sequencing project
Unpublished
2 (bases 1 to 1813)
Isogai,T. and Otsuki,T.
Direct Submission
Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
MEDO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; cDNA full insert
sequencing; Research Association for Biotechnology; cDNA library
construction, 5'- & 3'-end one pass sequencing and clone selection;
Helix Research Institute (supported by Japan Key Technology Center
etc.) and Department of Virology, Institute of Medical Science,
University of Tokyo.
FEATURES
source
location/Qualifiers
1..1813
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BASE COUNT 489 a 400 c 405 g 519 t
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Db 511 ATCTTCTGCTCTTTTCCCATCTTACCGGGGCTTGTGACCCCTGGCCATCCATC 570
OY 41 TTPATGLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHis 60
Db 571 TGGAGATTGAAGCCTTACGCTGACTGTGGCCCTTTTGCAGGCTGCTCTTCTTCAATC 630
OY 61 SerIleTySerTrpIleAspPheSerThrArgProGlyTyLeuTrpValValTrp 80
Db 631 TCCATCTACACCTGATGACACCTTAAGTACAGGCGCTGGCTACCTGCGGTTGTTGG 690
OY 81 IleTyArgAsnLeuIleGlySerValHisPhePheIleLeuThrLeuIleValLeu 100
Db 691 ATCATGCGGAACCTCATGTGAGAGTGCACCTCTTTTTCATCTCACCCTCATTTGTGCTA 750
OY 101 IleIleThrTyLeuTyTrpGlnIleThrGlnGlyArgGlyIleMetIleArgLeuLeu 120
Db 751 ATCATCACCCTATCTTACTGCGACATCAGAGAGAGAGAGATTAATATGAGGCTGCTC 810
OY 121 HisGlnGlnIleIleAsnGlnGlyLysAspLysMetPheLeuIleGlyLeuIleLys 140
Db 811 CATGACGAGATCATTAATGAGGCAAAAGATTAATGTTCCGATAGAAAATGATCAAG 870
OY 141 LeuGlnAspMetGlnLysLysAlaAsnProSerSerLeuValLeuGlnArgGlnVal 160
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OY 161 GlnGlnGlnGlyPheLeuHisLeuGlyGlnHisAspGlySerLeuAspLeuArgSerArg 180
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OY 181 ArgSerValGlnGlnGlyAsnProArgAla 190
Db 991 AGATCACTTCAGAGAGATTAATCCAGAGGCC 1020
RESULT 3
AX108538
LOCUS AX108538 1960 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 5 from Patent WO0123417.
ACCESSION AX108538
VERSION AX108538.1 GI:13923838
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1960)
AUTHORS Vinals y de Bassols,C.
TITLE Human tumor-associated lak-4p related polynucleotides and
polypeptides and their uses
JOURNAL Patent: WO 0123417-A 5 05-APR-2001;
SMITHKLINE BECHAM BIOLOGICALS S.A. (BE)
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Db 805 ATCTTCTGCTCTTTTCCCATCTTACCGGGGCTTGTGACCCCTGGCCATCCATC 864
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Db 865 TGGAGATTGAAGCCTTACGCTGACTGTGGCCCTTTTGCAGGCTGCTCTTCTTCAATC 924
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OY 141 LeuGlnAspMetGlnLysLysAlaAsnProSerSerLeuValLeuGlnArgGlnVal 160
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Db 1225 GAGACACAGAGCTTTTTCATTTTGGGGACATATGAGCACTTGACTTGCGATCTAGA 1284
OY 181 ArgSerValGlnGlnGlyAsnProArgAla 190
Db 1285 AGATCACTTCAGAGAGATTAATCCAGAGGCC 1314
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LOCUS AX108534 2407 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 1 from Patent WO0123417.
ACCESSION AX108534
VERSION AX108534.1 GI:13923834
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2407)
AUTHORS Vinals y de Bassols,C.
TITLE Human tumor-associated lak-4p related polynucleotides and
polypeptides and their uses
JOURNAL Patent: WO 0123417-A 1 05-APR-2001;
SMITHKLINE BECHAM BIOLOGICALS S.A. (BE)
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 REFERENCE
 AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 TITLE vinals y de Bassols, C.
 JOURNAL Human tumor-associated lak-4p related polynucleotides and
 peptides and their uses
 PATENT: WO 0123417-A 3 05-APR-2001;
 SMITHKLINE BEECHAM BIOLOGICALS S.A. (BE)
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 OY 81 lleYrArgAsnLeuIleGlySerValHisPhePhePheIleLeuThrLeuIleValleu 100
 DB 1546 ATCTATCGGAACCTCATGGAAGTGTGACCTTTTTCATCTTCACCTCATTTGTGCTA 1605
 OY 101 lleIleThrYrLeuYrTrpGlnIleThrGluGlyArgGlyIleMetIleArgLeuLeu 120
 DB 1606 ATCATCACCTATCTTTACTGGCAGATCACAGAGGAGAGAGATATATTAAGCTGCTC 1665
 OY 121 HisGluGlnIleIleAsnGluGlyLysAspLysMetPheLeuIleGluLysLeuIleLys 140
 DB 1666 CATGACGATCATTAATAGAGGCAAGATATAATGTTCCGTATGAATAATGATCAAG 1725
 OY 141 LeuGlnAspMetGluLysLysAlaAsnProSerSerLeuValLeuGluArgGluVal 160
 DB 1726 CTGACGATATGAG 1785
 OY 161 GluGlnGlnGlyPheLeuHisLeuGlyGlnHisAspGlySerLeuAspLeuArgSerArg 180
 DB 1786 GAGCAACAAGCCTTTTTCATTTGGGGGACATATGAGCAGTCTTGACTCGATCTAGA 1845
 OY 181 ArgSerValGlnGluGlyAsnProArgAla 190
 DB 1846 AGATCACTCAAGAGAGTAATCCAAAGGCC 1875
 RESULT 6
 BC027602
 LOCUS BC027602 2760 bp mRNA linear PRI 01-MAY-2002
 DEFINITION Homo sapiens, similar to RIKEN CDNA 4932443I108 gene, clone
 MGC:26648 IMAGE:4839111, mRNA, complete cds.
 ACCESSION BC027602
 VERSION BC027602.1 GI:20381190
 KEYWORDS
 SOURCE MGC.
 ORGANISM Homo sapiens.
 Homo sapiens.
 Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 AUTHORS Strausberg, R.
 TITLE Direct Submission
 JOURNAL Submitted (08-APR-2002) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2550,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgabs-r@mail.nih.gov
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 CDNA Library Preparation: Michael J. Brownstein (NHCRI) & Shitaki
 Toshiyuki and Ptero Carnuci (RIKEN)
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
 contact: amadansystemsbiology.org
 Anup Madan, Jessica Fahney, Erin Helton, Mark Ketteman, Anuradha
 Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
 Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LNLN at: <http://image.lnl.gov>
 Series: IRAK Plate: 34 Row: P Column: 13
 This clone was selected for full length sequencing because it

passed the following selection criteria: Genomescan gene prediction, Similarity but not identity to protein.
Location/Qualifiers
1. 2760

FEATURES
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/db_xref="taxon:9606"
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/tissue_type="testis"
/clone_lib="NH_MGC_97"
/lab_host="DH10B"
/note="Vector: pBluescript"
213..2495

CDS

/codon_start=1
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OGOKLASLIPMTSRDRIKAIKRNQPRMEKRLKRVKDEKSKQTRIIQLKNCIOC
LNSISAVRRKNSLSEISLSLWQKTLTIIGKRETSVLSFTNRLMLKNIFFS
ILNFSPIIIPQFVAKNTLQFTGLEFTGVYERDVMVYGEYTNLTGHSNGASY
NMOLAYFTIACLTTCFSLFSMAKYPNNFIPHISGSGITKLCFMDFTVTHK
AVLKQKNSLTERENISELROENSKLTFENOLBRSAYAVAWVSVIACCAAY
YLAENVLEPKTHSNPGAVILLPPVSCINLAVPCISMRILVEREMPRHEVYVILI
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RRTIGMQLITSLGLOEDIANVLELILYAGTLVWIGIFCPLPFIOMILFMEYSK
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LPLFHSIYSWIDTLSTRPGYLWVWVIRNLISVHFFLITLITLYIYMOITG
RKIMIRLHDOIINNEGDKMFLIKIKIDMKEMKAPSSVIVERRVEQGFHLHE
HDSIDLRSRASVSQENPRA"

BASE COUNT 739 a 637 c 625 g 759 t
ORIGIN

Alignment Scores:

Pred. No.: 4,696-189 Length: 2760
Score: 190.00 Matches: 190
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-895-298a-83 (1-190) x BC027602 (1-2760)

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DB 1923 ATGATGATTTCCAGCCCTCCAGCAAGCCGCGGCGCTCACAGATGATGACTTTC 1982
OY 21 IlePheLeuLeuPhePheProSerPheThrGlyValLeuGlySerThrLeuAlaIlePhe 40
DB 1983 ATCTCTTGCTCTTCTTCCCTTCCCTTCCGCGGCTTGTGTGACCTGCGCCATCCACATC 2042
OY 41 TrpArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHis 60
DB 2043 TGGAGATTGAAGCCTTCAGCTGACGTGCGCCCTTTTGGAGGCTGCCCTCTTCATTCAC 2102
OY 61 SerIleGlySerTrpIleAspThrLeuSerThrArgProGlyTrpLeuTrpValValTrp 80
DB 2103 TCCATCTACACCTGATGACACCTTAAGTACACGCGCTGCTGCTGCTGCTGCTTGG 2162
OY 81 IleLeuArgAsnLeuIleGlySerValHisPhePhePheIleLeuThrLeuIleValLeu 100
DB 2163 ATCTATCGGAACCTCATTTGGAAGTGTGCACTTCTTTCATCCCTCACCTCATTTGTGCTA 2222
OY 101 IleIleThrTrpLeuTrpTrpGlnIleThrGlnGlyArgGlyIleMetIleArgLeuLeu 120
DB 2223 ATCATCACCTTCTTACTGCAATCATCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2282
OY 121 HisGlnGlnIleIleAsnGlnGlyLysAspLysMetPheLeuIleGlnLysLeuIleLys 140
DB 2283 CATGAGCAGATCATTAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2342
OY 141 LeuGlnAspMetGlnLysLysAlaAsnProSerSerLeuValLeuGlnArgArgGlnVal 160

DB 2343 CTCGAGATATGAGGAAGAAAGCAAGCAAGCCAGCTACTGTTCTGGAAGAGAGAGGTG 2402

OY 161 GluGlnGlnGlyPheLeuHisLeuGlyGlnHisAspGlySerLeuAspLeuArgSerArg 180

DB 2403 GAGCAACAAGCCTTTTTCATTTGGGAGACATGATGACGCTGCTGCTGCTGCTGCTG 2462

OY 181 ArgSerValGlnGlnGlyLysAsnProArgAla 190

DB 2463 AGATCATGTTCAAGAGGATTAATCCAAAGGCGC 2492

RESULT 7

AK093944 2387 bp mRNA linear PRI 15-JUL-2002

LOCUS Homo sapiens cDNA FLJ36625 f1s, clone TRACH2017368, weakly similar

DEFINITION Homo sapiens mRNA for LAR-4p.

ACCESSION AK093944

VERSION AK093944.1 GI:21752906

KEYWORDS oligo capping: f1s (full insert sequence).

SOURCE Homo sapiens trachea cDNA to mRNA, clone lib:TRACH2

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Suzuki, O., Sasaki, N., Aotsuka, S., Shoji, T., Ichihara, T.,

Shiohata, N., Matsumoto, K., Hirano, M., Sano, S., Nomura, R.,

Yoshihara, Y., Matsumura, Y., Moriya, S., Chiba, E., Momiyama, H.,

Onogawa, S., Kaeriyama, S., Satoh, N., Matsunawa, H., Takahashi, E.,

Kataoka, R., Kuga, N., Kuroda, A., Satoh, I., Kamata, K., Takami, S.,

Terasima, Y., Watanabe, M., Sugiyama, T., Irie, R., Otsuki, T.,

Sato, H., Ota, T., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y.,

Kawai, H., O., Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H.,

Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K.,

Magatsuma, M., Murakawa, K., Kanehori, K., Takahashi, Fujii, A.,

Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S.,

Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T.

NEBO human cDNA sequencing project

Unpublished

2 (bases 1 to 2387)

Isogai, T. and Yamamoto, J.

Direct Submission

Submitted (04-JUL-2002) Takao Isogai, FUJ Project(HRI Team); 2-6-7

Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan Fax:81-438-52-3986)

(E-mail:genomc@hri.co.jp, Tel:81-438-52-3973, Fax:81-438-52-3986)

NEBO human cDNA sequencing project supported by Ministry of

Economy, Trade and Industry of Japan; cDNA full insert sequencing:

Research Association for Biotechnology (RAB); cDNA library

construction: Helix Research Institute (HRI) (supported by Japan

Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,

HRI, and Biotechnology Center, National Institute of Technology and

RAB; annotation: HRI and RAB.

RAB; annotation: clone selection for full insert sequencing: HRI and

RAB; annotation: clone selection for full insert sequencing: HRI and

RAB; annotation: clone selection for full insert sequencing: HRI and

RAB; annotation: clone selection for full insert sequencing: HRI and

QY 1 MetMetAspPheGlnProProSerLysAlaTrpArgAlaSerGlnMetThrPhe 20
 DB 1025 ATGATGANTTTCAGGCTTCGAGCAAGGCTGGGGCTCCAGATGATGACTTCTTC 1084
 QY 21 IlePheLeuLeuPhePheProSerPheThrGlyValLeuCySThrLeuAlaIleThrIle 40
 DB 1085 ATCTCTGCTCTTTCCTCCATCCTTCACCGGGCTCTTGTCAGCCCTGGCCATCCACATC 1144
 QY 41 TrpArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHis 60
 DB 1145 TGGAGATTGAAGCCCTTCAGCTGAGCTGGCCCTTTTCAGAGGCTGCCCTCTCTTCATTCAC 1204
 QY 61 SerIleTyrSerTrpIleAspThrLeuSerThrArgProGlyTyrLeuTrpValAlaTrp 80
 DB 1205 TCCTATCTACCTGATGACACCTTAAGTACAGGCTGCTGACCTGCTGCTGGGTGTTGG 1264
 QY 81 IleTyrArgAsnLeuIleGlySerValHisPhePheIleLeuThrLeuIleValLeu 100
 DB 1265 ATCTATGGAACCTCATTTGGAAGTGTGCTCTTTTCATCTCCACCTCATTTGTGCTA 1324
 QY 101 IleIleThrTyrLeuTyrTrpGlnIleThrGlyValArgLysIleMetIleArgLeuLeu 120
 DB 1325 ATCTATGACCTATCTTCTTACTGACATCAGAGGAGGAGGAGATTAATGATTAAGGCTGCTC 1384
 QY 121 HisGlnGlnIleIleAsnGlnGlyLysAspLysMetPheLeuIleGlu-LysLeuIleLys 140
 DB 1385 CATGAGACGATCATTAATGAGGCAAGATTAATGTTCTGTGATAGG-AAAATGATCA 1443
 QY 140 sleuGlnAspMetGlnLysLysAlaAsnProSerSerLeuValLeuLysArgGluVal 160
 DB 1444 GCTGAGAGATATGAG 1503
 QY 160 IGIuGlnGlnGlyPheLeuHisLeuGlyLysLysAspGlySerLeuAspLeuArgSer 180
 DB 1504 GGGAGCAACAGGCTTTTGGATTTGGGGGAGACATGATGAGCTTGTGCTGCTGCTAG 1563
 QY 180 GARGSerValGlnGlnGlyLysProArgAla 190
 DB 1564 AAGATCATGTTCAAGAGATATCAAGAGGCT 1594
 RESULT 8
 AK097718
 LOCUS
 DEFINITION Homo sapiens CDNA FLJ40399 fls, clone TEST12037081, weakly similar
 to Homo sapiens mRNA for IAK-4p.
 AK097718
 VERSION AK097718.1 GI:21757573
 KEYWORDS oligo capping; fls (full insert sequence);
 SOURCE Homo sapiens testis CDNA to mRNA, clone_id:TEST12
 ORGANSIM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1
 Oshima, A., Takahashi, Fujii, A., Tanase, T., Imose, N., Takeuchi, K.,
 Arita, M., Mutsashino, K., Yuki, H., Hara, H., Sugiyama, T., Irie, R.,
 Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y.,
 Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K.,
 Magatsuma, M., Murakawa, K., Kanehori, K., Sugiyama, A., Kawakami, B.,
 Suzuki, Y., Sugano, S., Nagahara, K., Masuho, Y., Nagai, K. and
 Isogai, T.
 NEDO human cDNA sequencing project
 Unpublished
 2 (bases 1 to 2399)
 Isogai, T. and Yamamoto, J.
 Direct Submission
 Submitted (04-JUL-2002) Takao Isogai, Fij Project (HRI Team); 2-6-7
 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
 (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
 NEDO human cDNA sequencing project supported by Ministry of
 Economy, Trade and Industry of Japan; cDNA full insert sequencing;
 Research Association for Biotechnology (RAB); cDNA library

FEATURES
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 /db_xref="taxon:9606"
 /clone="TEST12037081"
 /tissue="testis"
 /clone_lib="TEST12"
 /note="Cloning vector: pME18SFL3"
 BASE COUNT 610 a 591 c 528 g 670 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 5.37e-122 Length: 2399
 Score: 126.00 Matches: 126
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 66.32% Indels: 0
 DB: 9 Gaps: 0
 US-09-895-298a-83 (1-190) x AK097718 (1-2399)
 QY 1 MetMetAspPheGlnProProSerLysAlaTrpArgAlaSerGlnMetThrPhe 20
 DB 1933 ATGATGANTTTCAGGCTTCGAGCAAGGCTGGGGCTCCAGATGATGACTTCTTC 1992
 QY 21 IlePheLeuLeuPhePheProSerPheThrGlyValLeuCySThrLeuAlaIleThrIle 40
 DB 1993 ATCTCTGCTCTTTCCTCCATCCTTCACCGGGCTCTTGTCAGCCCTGGCCATCCATC 2052
 QY 41 TrpArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHis 60
 DB 2053 TGGAGATTGAAGCCCTTCAGCTGAGCTGGCCCTTTTCAGAGCTGCTGCTCATTTGCTAC 2112
 QY 61 SerIleTyrSerTrpIleAspThrLeuSerThrArgProGlyTyrLeuTrpValAlaTrp 80
 DB 2113 TCCTATCTACCTGATGACACCTTAAGTACAGGCTGCTGCTGGGTGTTGG 2172
 QY 81 IleTyrArgAsnLeuIleGlySerValHisPhePheIleLeuThrLeuIleValLeu 100
 DB 2173 ATCTATGGAACCTCATTTGGAAGTGTGCTCTTTTCATCTCCACCTCATTTGTGCTA 2232
 QY 101 IleIleThrTyrLeuTyrTrpGlnIleThrGlyValArgLysIleMetIleArgLeuLeu 120
 DB 2233 ATCTATGACCTATCTTCTTACTGACATCAGAGGAGGAGGAGATTAATGATTAAGGCTGCTC 2292
 QY 121 HisGlnGlnIleIleAsn 126
 DB 2293 CATGAGCAGATCATTAAT 2310
 RESULT 9
 HU091321
 LOCUS
 DEFINITION Human Chromosome 16 BAC clone CIT9878-A-363E6, complete sequence.
 ACCESSION U91321
 VERSION U91321.1 GI:2951946
 KEYWORDS HFG
 ORGANSIM Homo sapiens
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 220633)
 Loftus, B.J., Kim, D.J., Sneddon, V.P., Kalush, F., Brandon, R.,
 Fuhrmann, J., Mason, T., Crosby, M.L., Barnstead, M., Cronin, L.,
 Eichler, E.E., Harris, P.C., Venter, J.C. and Adams, M.D.
 Genome duplications and other features in 12 Mb of DNA sequence
 from human chromosome 16p and 16q
 Genomics 60 (3), 295-308 (1999)


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MEDLINE      99425270
* PUBMED    10493829
REFERENCE    2 (bases 1 to 220633)
AUTHORS      Adams,M.D., Loftus,B.J., Phillips,C.A., Zhou,L., Brandon,R.,
              Fuhrmann,J. and Venter,J.C.
TITLE        Direct Submission
JOURNAL      Submitted (04-MAR-1997) The Institute for Genomic Research, 9712
              Medical Center Dr., Rockville, MD 20850, USA
REFERENCE    3 (bases 1 to 220633)
AUTHORS      Adams,M.D., Loftus,B.J., Zhou,L. and Labombard,M.
TITLE        Direct Submission
JOURNAL      Submitted (21-MAY-1997)
              4 (bases 1 to 220633)
AUTHORS      Adams,M.D., Loftus,B.J., Zhou,L., La Bombard,M., Kim,U.J. and
              Venter,J.C.
TITLE        Direct Submission
JOURNAL      Submitted (19-AUG-1997) The Institute for Genomic Research, 9712
              Medical Center Dr., Rockville, MD 20850, USA
REFERENCE    5 (bases 1 to 220633)
AUTHORS      Adams,M.D., Loftus,B.J., Zhou,L., La Bombard,M., Kim,U.J. and
              Venter,J.C.
TITLE        Direct Submission
JOURNAL      Submitted (22-AUG-1997) The Institute for Genomic Research, 9712
              Medical Center Dr., Rockville, MD 20850, USA
REFERENCE    6 (bases 1 to 220633)
AUTHORS      Adams,M.D.
TITLE        Direct Submission
JOURNAL      Submitted (11-MAR-1998) The Institute for Genomic Research, 9712
              Medical Center Dr., Rockville, MD 20850, USA
COMMENT      On Mar 11, 1998 this sequence version replaced g1:2335062.
              BAC clone CIT987SK-363E6 is located in band 16p13.1 of chromosome
              16. Genes were identified by anonymous ftp from arthur.epm.ornl.gov),
              XGRALT (available by anonymous ftp from
              collinsu.washington.edu), GENSCAN (available using the e-mail server
              at genescan.genomic.stanford.edu), searches of the EST database at
              TIGR (http://www.tigr.org/tdb/hcd/hcd.html) and searches against a
              peptide database. Repeats were identified using RepeatMasker (Smilt,
              A.F.A. and Green, P. unpublished,
              http://ftp.genome.washington.edu/rm/RepeatMasker.html).
              location/Qualifiers
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              TIMAAPSAFLE"
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ORIGIN
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Pred. No.: 3,89e-50
Score: 59.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 31.05%
DB: 9
US-09-895-298A-83 (1-190) x HU091321 (1-220633)
OY 42 ArgleuysProSerAlaAspCysGlyProPhaArgGlyLeuProLeuPhelHisSer 61
Db 20486 AGATTGAAGCCTTCAGCTGAGTGGCCCTTTGAGAGTGGCTCTCTTATTCACCTCC 204925
OY 62 IleTyrSerTrpIleAspThrLeuSerThrArpProGlyTyrLeuTrpValValTrpIle 81
Db 204926 ATCTACAGCTGATCGATCGACCCCTAAGTACAGCGCTGCTACCTGGTGTGGATC 204985
OY 82 TyrArgAsnLeuIleGlySerValHisPhePheIleLeuThrLeuIleValLeu 100
Db 204986 TATCGAACCCTCATTTGGAAGTGTGCACCTCTTTTCATCTCCACCCCTCATTTGCTGTG 205042
RESULT 10
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LOCUS Homo sapiens chromosome 16 clone CTA-363E6, WORKING DRAFT SEQUENCE,
DEFINITION 5 unordered pieces.
ACCESSION AC130456
VERSION AC130456.1 GI:22203229
KEYWORDS HTG; HTGS-PHASE1; HTGS-DRAFT; HTGS-ACTIVERIN.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 223280)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 16
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 223280)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (10-AUG-2002) Production Sequencing Facility, DOE Joint
              Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT -----Genome Center
              Center: Joint Genome Institute
              Center Code: JGI
              Web site: http://www.jgi.doe.gov
              -----
              Project Information
              Center Project Name: 2773242
              Center clone name: CIT978SKA_363E6
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              Consensus quality: 221100 bases at least Q40
              Consensus quality: 222027 bases at least Q30
              Consensus quality: 222494 bases at least Q20
              Estimated insert size: 220633; agarose-fp estimation
              Quality coverage: 10.81 in Q20 bases; agarose-fp estimation
              Quality coverage: 10.71 in Q20 bases; sum-of-contigs estimation
              NOTE: This is a 'working draft' sequence. It currently
              consists of 5 contigs. The true order of the pieces
              is not known and their order in this sequence record is
              arbitrary. Gaps between the contigs are represented as
              runs of N, but the exact sizes of the gaps are unknown.
              * This record will be updated with the finished sequence
              * as soon as it is available and the accession number will
              be preserved.
              1 1261: contig of 1261 bp in length
              * 1262 1361: gap of unknown length
              * 1362 2690: contig of 1329 bp in length

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BASE COUNT 45464 a 34232 c 36100 g 48768 t
ORIGIN

Alignment Scores:

Pred. No.: 4,49e-25 Length: 164564
Score: 35.00 Matches: 35
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 18.42% Indels: 0
DB: 9 Gaps: 0

US-09-895-298A-83 (1-190) x HUCAC003108 (1-164564)

OY 127 GluGlyLysAspLysMetPheLeuIleGluLysLeuIleLysLeuGlnAspMetGluLys 146

DB 1200 GAGGGCAAGATGATAAATGTCCTGATGAAAAATGATCAACGTCGACGATATGAGAG 1259

OY 147 LysAlaAspProSerSerLeuValLeuGluLysArgGluValGlu 161

DB 1260 AATCAACAAACCCACGCTCTGTTCTGGAAGAGAGAGGTGGAG 1304

RESULT 12

AC124444_2/c

WPCOMMENT

Sequence split into 5 fragments LOCUS AC124444 Accession AC124444

Fragment Name

AC124444_0

AC124444_1

AC124444_2

AC124444_3

AC124444_4

Continuation (3 of 5) of AC124444 from base 200001 (AC124444 Mus musculus chromosome UNK

Alignment Scores:

Pred. No.: 9.89e-15 Length: 110000
Score: 25.00 Matches: 25
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 13.16% Indels: 0
DB: 2 Gaps: 0

US-09-895-298A-83 (1-190) x AC124444_2 (1-110000)

OY 18 ThrPhePheIlePheLeuLeuPheProSerPheThrGlyValLeuGlyTyrLeuAla 37

DB 84639 ACTTCTTCATTTCTCTCTCTCCATCTTCACGGAGTCTGTGACACCTGGCT 84640

OY 38 IleThrIleTyrArg 42

DB 84639 ATCACCATCTGGAG 84625

RESULT 13

MMU297000

LOCUS MMU297000 623 bp DNA linear ROD 15-NOV-2001

DEFINITION Mus musculus SDS-stable vimentin-bound DNA fragment MEF10VIMB9.

ACCESSION AJ297000.1 GI:10047031

VERSION AJ297000.1

KEYWORDS vimentin.

SOURCE house mouse.

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

TITLE

1 Tolstong, G.V., Mothes, E., Shoeman, R.L. and Traub, P.

Isolation of SDS-Stable Complexes of the Intermediate Filament

Protein Vimentin with Repetitive, Mobile, Nuclear Matrix Attachment

Region, and Mitochondrial DNA Sequence Elements from Cultured Mouse

and Human Fibroblasts

JOURNAL DNA Cell Biol. 20 (9), 531-554 (2001)

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

SUBMITTED

Zellbiologie

Rosenthal

Jadenburg

Heidelberg

68526

Germany

Location/Qualifiers

source

1. 623

/organism="Mus musculus"

/db_xref="taxon:10090"

/cell_type="senescent mouse embryo fibroblasts"

/clone_lib="MEF10VIMB9"

1. 623

/bound_moiety="vimentin"

/function="sequence bound by vimentin in living cells"

repeat_region

346..623

/rpt_family="MADR"

BASE COUNT

140 a 157 c 167 g 159 t

ORIGIN

Alignment Scores:

Pred. No.: 3.15e-09 Length: 623
Score: 18.00 Matches: 18
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.47% Indels: 0
DB: 10 Gaps: 0

US-09-895-298A-83 (1-190) x MMU297000 (1-623)

OY 25 PhePheProSerPheThrGlyValLeuGlyThrLeuAlaIleThrTyrArg 42

DB 197 TTCTTCCATCTTCACGGAGTGTGTGACACCTGTATCACCATCTGGAG 250

RESULT 14

AC100877

LOCUS

DEFINITION

AC100877

ACCESSION

VERSION

KEYWORDS

HTG: HTGS, PHASEO.

Mus musculus.

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 71596)

2 (bases 1 to 71596)

unpublished

unpublished

unpublished

unpublished

unpublished

unpublished

unpublished

unpublished

unpublished

unpublished

unpublished

unpublished

unpublished

unpublished

TITLE
JOURNAL
COMMENT

Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D.,
Oliver, P., Peterson, K., Phunkhang, P., Pierre, N., Pollara, A.,
Raymond, C., Rella, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,
Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schnepfack, R.,
Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Straus, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J.,
Topham, K., Travers, M., Trivas, N., Triggillo, D., Vassiliou, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
Smt. A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: MIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

Project Information

Center project name: I13918

Center clone name: 35_B_17

* NOTE: This record contains 87 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

1 722: contig of 722 bp in length
* 723 822: gap of 100 bp
* 823 1526: contig of 704 bp in length
* 1527 1626: gap of 100 bp
* 1627 2436: contig of 710 bp in length
* 2437 3156: contig of 720 bp in length
* 3157 3256: gap of 100 bp
* 3257 3984: contig of 728 bp in length
* 3985 4084: gap of 100 bp
* 4085 4811: contig of 727 bp in length
* 4812 4911: gap of 100 bp
* 4912 5638: contig of 727 bp in length
* 5639 5738: gap of 100 bp
* 5739 6477: contig of 739 bp in length
* 6478 6577: gap of 100 bp
* 6578 7305: contig of 728 bp in length
* 7306 7405: gap of 100 bp
* 7406 8107: contig of 702 bp in length
* 8108 8207: gap of 100 bp
* 8208 8950: contig of 743 bp in length
* 8951 9050: gap of 100 bp
* 9051 9743: contig of 693 bp in length
* 9744 9843: gap of 100 bp
* 9844 10583: contig of 740 bp in length
* 10584 10683: gap of 100 bp
* 10684 11405: contig of 722 bp in length
* 11406 11505: gap of 100 bp
* 11506 12236: contig of 731 bp in length
* 12237 12336: gap of 100 bp
* 12337 13069: contig of 733 bp in length
* 13070 13169: gap of 100 bp
* 13170 13851: contig of 682 bp in length
* 13852 13951: gap of 100 bp
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* 15513 15612: gap of 100 bp

15613 16342: contig of 730 bp in length
* 16343 16442: gap of 100 bp
* 16443 17175: contig of 733 bp in length
* 17176 17275: gap of 100 bp
* 17276 17973: contig of 698 bp in length
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* 18074 18798: contig of 725 bp in length
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* 19723 20437: contig of 715 bp in length
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* 21367 22094: contig of 728 bp in length
* 22095 22194: gap of 100 bp
* 22195 22903: contig of 709 bp in length
* 22904 23003: gap of 100 bp
* 23004 23745: contig of 742 bp in length
* 23746 23845: gap of 100 bp
* 23846 24584: contig of 739 bp in length
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* 25328 25427: gap of 100 bp
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* 26145 26244: gap of 100 bp
* 26245 26977: contig of 733 bp in length
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* 27777 27876: gap of 100 bp
* 27877 28595: contig of 719 bp in length
* 28596 28695: gap of 100 bp
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* 31170 31896: contig of 727 bp in length
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* 34507 35237: contig of 731 bp in length
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* 36166 36880: contig of 715 bp in length
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* 37695 37794: gap of 100 bp
* 37795 38521: contig of 727 bp in length
* 38522 38621: gap of 100 bp
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* 39350 39449: gap of 100 bp
* 39450 40190: contig of 741 bp in length
* 40191 40290: gap of 100 bp
* 40291 41012: contig of 722 bp in length
* 41013 41112: gap of 100 bp
* 41113 41852: contig of 740 bp in length
* 41853 41952: gap of 100 bp
* 41953 42688: contig of 736 bp in length
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* 42789 43523: contig of 735 bp in length
* 43524 43623: gap of 100 bp
* 43624 44318: contig of 695 bp in length
* 44319 44418: gap of 100 bp
* 44419 45138: contig of 720 bp in length
* 45139 45238: gap of 100 bp
* 45239 45976: contig of 738 bp in length

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* 45977 46076: gap of 100 bp
* 46077 46808: contig of 732 bp in length
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* 47614 47713: gap of 100 bp
* 47714 48431: contig of 718 bp in length
* 48432 48531: gap of 100 bp
* 48532 49280: contig of 749 bp in length
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* 49381 50139: contig of 759 bp in length
* 50140 50239: gap of 100 bp
* 50240 50966: contig of 727 bp in length
* 50967 51066: gap of 100 bp
* 51067 51797: contig of 731 bp in length
* 51798 51897: gap of 100 bp
* 51898 52632: contig of 735 bp in length
* 52633 52732: gap of 100 bp
* 52733 53448: contig of 716 bp in length
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* 53549 54266: contig of 718 bp in length
* 54267 54366: gap of 100 bp
* 54367 55107: contig of 741 bp in length
* 55108 55207: gap of 100 bp
* 55208 55927: contig of 720 bp in length
* 55928 56027: gap of 100 bp
* 56028 56757: contig of 730 bp in length
* 56758 56857: gap of 100 bp

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Alignment Scores:

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Pred. No.: 1.7e-06 Length: 71596
Score: 17.00 Matches: 17
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.95% Indels: 0
DB: 2 Gaps: 0

```

US-09-895-298a-83 (1-190) x AC100877 (1-71596)

QY 84 AsnLeuIleGlySerValHisPhePhePheIleuIleuValLeu 100
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 Db 48783 AATCTCATTTGGAAGTGTGCACCTCTTCTTCATCTCCACCCCATGTGCTG 48833

RESULT 15
 AX071021 402 bp DNA linear PAT 25-JAN-2001
 LOCUS Sequence 1493 from Patent WO0102568.
 DEFINITION AX071021
 ACCESSION AX071021
 VERSION AX071021.1 GI:12581294
 KEYWORDS
 SOURCE human
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS
 1 (bases 1 to 402)
 Williams, L.T., Escobedo, J., Innis, M.A., Garcia, P.D., Klinger, J.,
 Kassam, A., Reinhard, C., Randazzo, F., Kennedy, G.C., Pot, D.,
 Lamson, G., Drmanac, R., Crkenjakov, R., Drmanac, S., Dickson, M.,
 Labat, I., Ieshkovitiz, D., Kita, D., Garcia, V. and Strache-Crain, B.
 Human genes and gene expression products
 Patent: WO 0102568-A 1493 11-JAN-2001;
 CHIRON CORPORATION (US) ; HYSEQ, INC. (US)

TITLE
 JOURNAL
 FEATURES
 source
 1..402
 Location/Qualifiers
 misc_feature
 1..402
 /db_xref="taxon:9606"
 /note="n = A,T,C or G"

BASE COUNT 83 a 106 c 87 g 124 t 2 others
 ORIGIN

Alignment Scores:
 Pred. No.: 2.75e-07 Length: 402
 Score: 16.00 Matches: 16

```

Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.42% Indels: 0
DB: 6 Gaps: 0

```

US-09-895-298a-83 (1-190) x AX071021 (1-402)

QY 1 MetMetAsnPhgGlnProProSerLysAlaTrpArgAlaSerGlnMet 16
 |||||||
 Db 269 ATGATGAATTTCACGCTCCGAGCAAGCGCTGCGGCTCAGAGATG 316

Search completed: November 9, 2002, 08:33:48
 Job time : 2869 secs

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